

SEQUENCE LISTING

<110> SunGene GmbH & Co.KGaA

<120> Overexpression of a DNA sequence encoding a
2-methyl-6-phytylhydroquinone methyltransferase in
plants.

<130> MPMTSynechocystis

<140>

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<160> 10

<170> PatentIn Vers. 2.0

<210> 1

<211> 957

<212> DNA

<213> Synechocystis PCC6803

<220>

<221> CDS

<222> (1)..(957)

<400> 1

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1				5					10					15		

gcg	atc	gcc	gct	gga	ctg	tat	ctc	cta	act	gcc	cgg	ggc	tat	cag	tca	96
Ala	Ile	Ala	Ala	Gly	Leu	Tyr	Leu	Leu	Thr	Ala	Arg	Gly	Tyr	Gln	Ser	
			20					25					30			

tcg	gat	tcc	gtg	gcc	aac	gcc	tac	gac	caa	tgg	aca	gag	gac	ggc	att	144
Ser	Asp	Ser	Val	Ala	Asn	Ala	Tyr	Asp	Gln	Trp	Thr	Glu	Asp	Gly	Ile	
		35					40					45				

ttg	gaa	tat	tac	tgg	ggc	gac	cat	atc	cac	ctc	ggc	cat	tat	ggc	gat	192
Leu	Glu	Tyr	Tyr	Trp	Gly	Asp	His	Ile	His	Leu	Gly	His	Tyr	Gly	Asp	
	50				55						60					

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Pro	Pro	Val	Ala	Lys	Asp	Phe	Ile	Gln	Ser	Lys	Ile	Asp	Phe	Val	His	
65					70					75				80		

gcc	atg	gcc	cag	tgg	ggc	gga	tta	gat	aca	ctt	ccc	ccc	ggc	aca	acg	288
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Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr Thr	
85 90 95	
gta ttg gat gtg ggt tgc ggc att ggc ggt agc agt cgc att ctc gcc	336
Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu Ala	
100 105 110	
aaa gat tat ggt ttt aac gtt acc ggc atc acc att agt ccc caa cag	384
Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro Gln Gln	
115 120 125	
gtg aaa cgg gcg acg gaa tta act cct ccc gat gtg acg gcc aag ttt	432
Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala Lys Phe	
130 135 140	
gcg gtg gac gat gct atg gct ttg tct ttt cct gac ggt agt ttc gac	480
Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe Asp	
145 150 155 160	
gta gtt tgg tcg gtg gaa gca ggg ccc cac atg cct gac aaa gct gtg	528
Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala Val	
165 170 175	
ttt gcc aag gaa tta ctg cgg gtc gtg aaa cca ggg ggc att ctg gtg	576
Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile Leu Val	
180 185 190	
gtg gcg gat tgg aat caa cgg gac gat cgc caa gtg ccc ctc aac ttc	624
Val Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu Asn Phe	
195 200 205	
tgg gaa aaa cca gtg atg cga caa ctg ttg gat caa tgg tcc cac cct	672
Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser His Pro	
210 215 220	
gcc ttt gcc agc att gaa ggt ttt gcg gaa aat ttg gaa gcc acg ggt	720
Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala Thr Gly	
225 230 235 240	
ttg gtg gag ggc cag gtg act act gct gat tgg act gta ccg acc ctc	768
Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr Leu	
245 250 255	
ccc gct tgg ttg gat acc att tgg cag ggc att atc cgg ccc cag ggc	816
Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro Gln Gly	
260 265 270	
tgg tta caa tac ggc att cgt ggg ttt atc aaa tcc gtg cgg gaa gta	864

Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu Val
 275 280 285

ccg act att tta ttg atg cgc ctt gcc ttt ggg gta gga ctt tgt cgc 912
 Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu Cys Arg
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<210> 2

<211> 318

<212> PRT

<213> Synechocystis PCC6803

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 20 25 30

Ser Asp Ser Val Ala Asn Ala Tyr Asp Gln Trp Thr Glu Asp Gly Ile
 35 40 45

Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr Gly Asp
 50 55 60

Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val His
 65 70 75 80

Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr Thr
 85 90 95

Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu Ala
 100 105 110

Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro Gln Gln
 115 120 125

Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala Lys Phe
 130 135 140

Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe Asp
 145 150 155 160

Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala Val
165 170 175

Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile Leu Val
180 185 190

Val Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu Asn Phe
195 200 205

Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser His Pro
210 215 220

Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala Thr Gly
225 230 235 240

Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr Leu
245 250 255

Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro Gln Gly
260 265 270

Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu Val
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Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu Cys Arg
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Phe Gly Met Phe Lys Ala Val Arg Lys Asn Ala Thr Gln Ala
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<211> 974

<212> DNA

<213> Synechocystis PCC6803

<220>

<221> CDS

<222> (7)..(963)

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Ser Leu Ala Ile Ala Ala Gly Leu Tyr Leu Leu Thr Ala Arg Gly Tyr
15 20 25 30

cag tca tcg gat tcc gtg gcc aac gcc tac gac caa tgg aca gag gac	144
Gln Ser Ser Asp Ser Val Ala Asn Ala Tyr Asp Gln Trp Thr Glu Asp	
35 40 45	
ggc att ttg gaa tat tac tgg ggc gac cat atc cac ctc ggc cat tat	192
Gly Ile Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr	
50 55 60	
ggc gat ccg cca gtg gcc aag gat ttc atc caa tcg aaa att gat ttt	240
Gly Asp Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe	
65 70 75	
gtc cat gcc atg gcc cag tgg ggc gga tta gat aca ctt ccc ccc ggc	288
Val His Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly	
80 85 90	
aca acg gta ttg gat gtg ggt tgc ggc att ggc ggt agc agt cgc att	336
Thr Thr Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile	
95 100 105 110	
ctc gcc aaa gat tat ggt ttt aac gtt acc ggc atc acc att agt ccc	384
Leu Ala Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro	
115 120 125	
caa cag gtg aaa cgg gcg acg gaa tta act cct ccc gat gtg acg gcc	432
Gln Gln Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala	
130 135 140	
aag ttt gcg gtg gac gat gct atg gct ttg tct ttt cct gac ggt agt	480
Lys Phe Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser	
145 150 155	
ttc gac gta gtt tgg tcg gtg gaa gca ggg ccc cac atg cct gac aaa	528
Phe Asp Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys	
160 165 170	
gct gtg ttt gcc aag gaa tta ctg cgg gtc gtg aaa cca ggg ggc att	576
Ala Val Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile	
175 180 185 190	
ctg gtg gtg gcg gat tgg aat caa cgg gac gat cgc caa gtg ccc ctc	624
Leu Val Val Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu	
195 200 205	
aac ttc tgg gaa aaa cca gtg atg cga caa ctg ttg gat caa tgg tcc	672
Asn Phe Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser	
210 215 220	

cac cct gcc ttt gcc agc att gaa ggt ttt gcg gaa aat ttg gaa gcc	720
His Pro Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala	
225 230 235	
acg ggt ttg gtg gag ggc cag gtg act act gct gat tgg act gta ccg	768
Thr Gly Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro	
240 245 250	
acc ctc ccc gct tgg ttg gat acc att tgg cag ggc att atc cgg ccc	816
Thr Leu Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro	
255 260 265 270	
cag ggc tgg tta caa tac ggc att cgt ggg ttt atc aaa tcc gtg cgg	864
Gln Gly Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg	
275 280 285	
gaa gta ccg act att tta ttg atg cgc ctt gcc ttt ggg gta gga ctt	912
Glu Val Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu	
290 295 300	
tgt cgc ttc ggt atg ttc aaa gca gtg cga aaa aac gcc act caa gct	960
Cys Arg Phe Gly Met Phe Lys Ala Val Arg Lys Asn Ala Thr Gln Ala	
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taa attgcggatc c	974

<210> 4

<211> 318

<212> PRT

<213> Synechocystis PCC6803

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Met Pro Glu Tyr Leu Leu Leu Pro Ala Gly Leu Ile Ser Leu Ser Leu
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Ser Asp Ser Val Ala Asn Ala Tyr Asp Gln Trp Thr Glu Asp Gly Ile
35 40 45

Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr Gly Asp
50 55 60

Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val His

65					70						75				80
Ala	Met	Ala	Gln	Trp	Gly	Gly	Leu	Asp	Thr	Leu	Pro	Pro	Gly	Thr	Thr
				85					90					95	
Val	Leu	Asp	Val	Gly	Cys	Gly	Ile	Gly	Gly	Ser	Ser	Arg	Ile	Leu	Ala
			100					105					110		
Lys	Asp	Tyr	Gly	Phe	Asn	Val	Thr	Gly	Ile	Thr	Ile	Ser	Pro	Gln	Gln
		115					120					125			
Val	Lys	Arg	Ala	Thr	Glu	Leu	Thr	Pro	Pro	Asp	Val	Thr	Ala	Lys	Phe
	130					135					140				
Ala	Val	Asp	Asp	Ala	Met	Ala	Leu	Ser	Phe	Pro	Asp	Gly	Ser	Phe	Asp
145					150					155					160
Val	Val	Trp	Ser	Val	Glu	Ala	Gly	Pro	His	Met	Pro	Asp	Lys	Ala	Val
			165					170					175		
Phe	Ala	Lys	Glu	Leu	Leu	Arg	Val	Val	Lys	Pro	Gly	Gly	Ile	Leu	Val
		180						185					190		
Val	Ala	Asp	Trp	Asn	Gln	Arg	Asp	Asp	Arg	Gln	Val	Pro	Leu	Asn	Phe
		195					200					205			
Trp	Glu	Lys	Pro	Val	Met	Arg	Gln	Leu	Leu	Asp	Gln	Trp	Ser	His	Pro
	210					215					220				
Ala	Phe	Ala	Ser	Ile	Glu	Gly	Phe	Ala	Glu	Asn	Leu	Glu	Ala	Thr	Gly
225					230					235					240
Leu	Val	Glu	Gly	Gln	Val	Thr	Thr	Ala	Asp	Trp	Thr	Val	Pro	Thr	Leu
			245					250					255		
Pro	Ala	Trp	Leu	Asp	Thr	Ile	Trp	Gln	Gly	Ile	Ile	Arg	Pro	Gln	Gly
		260						265					270		
Trp	Leu	Gln	Tyr	Gly	Ile	Arg	Gly	Phe	Ile	Lys	Ser	Val	Arg	Glu	Val
		275					280					285			
Pro	Thr	Ile	Leu	Leu	Met	Arg	Leu	Ala	Phe	Gly	Val	Gly	Leu	Cys	Arg
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tca tcg gat tcc gtg gcc aac gcc tac gac caa tgg aca gag gac ggc 99
 Ser Ser Asp Ser Val Ala Asn Ala Tyr Asp Gln Trp Thr Glu Asp Gly
 15 20 25 30

att ttg gaa tat tac tgg ggc gac cat atc cac ctc ggc cat tat ggc 147
 Ile Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr Gly
 35 40 45

gat ccg cca gtg gcc aag gat ttc atc caa tcg aaa att gat ttt gtc	195
Asp Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val	
50 55 60	
cat gcc atg gcc cag tgg ggc gga tta gat aca ctt ccc ccc ggc aca	243
His Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr	
65 70 75	
acg gta ttg gat gtg ggt tgc ggc att ggc ggt agc agt cgc att ctc	291
Thr Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu	
80 85 90	
gcc aaa gat tat ggt ttt aac gtt acc ggc atc acc att agt ccc caa	339
Ala Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro Gln	
95 100 105 110	
cag gtg aaa cgg gcg acg gaa tta act cct ccc gat gtg acg gcc aag	387
Gln Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala Lys	
115 120 125	
ttt gcg gtg gac gat gct atg gct ttg tct ttt cct gac ggt agt ttc	435
Phe Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe	
130 135 140	
gac gta gtt tgg tcg gtg gaa gca ggg ccc cac atg cct gac aaa gct	483
Asp Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala	
145 150 155	
gtg ttt gcc aag gaa tta ctg cgg gtc gtg aaa cca ggg ggc att ctg	531
Val Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile Leu	
160 165 170	
gtg gtg gcg gat tgg aat caa cgg gac gat cgc caa gtg ccc ctc aac	579
Val Val Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu Asn	
175 180 185 190	
ttc tgg gaa aaa cca gtg atg cga caa ctg ttg gat caa tgg tcc cac	627
Phe Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser His	
195 200 205	
cct gcc ttt gcc agc att gaa ggt ttt gcg gaa aat ttg gaa gcc acg	675
Pro Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala Thr	
210 215 220	
ggg ttg gtg gag ggc cag gtg act act gct gat tgg act gta ccg acc	723
Gly Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr	
225 230 235	

ctc ccc gct tgg ttg gat acc att tgg cag ggc att atc cgg ccc cag 771
 Leu Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro Gln
 240 245 250

ggc tgg tta caa tac ggc att cgt ggg ttt atc aaa tcc gtg cgg gaa 819
 Gly Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu
 255 260 265 270

gta ccg act att tta ttg atg cgc ctt gcc ttt ggg gta gga ctt tgt 867
 Val Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu Cys
 275 280 285

cgc ttc ggt atg ttc aaa gca gtg cga aaa aac gcc act caa gct taa 915
 Arg Phe Gly Met Phe Lys Ala Val Arg Lys Asn Ala Thr Gln Ala
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<213> Synechocystis PCC6803

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Met Ala Ala Gly Leu Tyr Leu Leu Thr Ala Arg Gly Tyr Gln Ser Ser
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Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr Gly Asp Pro
 35 40 45

Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val His Ala
 50 55 60

Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr Thr Val
 65 70 75 80

Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu Ala Lys
 85 90 95

Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro Gln Gln Val
 100 105 110

Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala Lys Phe Ala
 115 120 125

Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe Asp Val
 130 135 140

Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala Val Phe
 145 150 155 160

Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile Leu Val Val
 165 170 175

Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu Asn Phe Trp
 180 185 190

Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser His Pro Ala
 195 200 205

Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala Thr Gly Leu
 210 215 220

Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr Leu Pro
 225 230 235 240

Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro Gln Gly Trp
 245 250 255

Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu Val Pro
 260 265 270

Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu Cys Arg Phe
 275 280 285

Gly Met Phe Lys Ala Val Arg Lys Asn Ala Thr Gln Ala
 290 295 300

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<212> DNA

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gtcgacctta agaatttaag cttgagtggc g

31